



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 114183

TO: Minh-Tam Davis
Location: rem/3a24/3c18
Art Unit: 1642
Wednesday, February 18, 2004

Case Serial Number: 10/023182

From: Toby Port
Location: Biotech-Chem Library
Remsen 1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Davis,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 17, 2004, 17:05:49 ; Search time 3057 Seconds

(without alignments)
10063.474 Million cell updates/sec

Title: US-10-023-182-1

Perfect score: 752

Sequence: 1 ATCTCTGAGGCGCTGACCT.....TAAACTGAGCTACGAAAA 752

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 2045481386 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1520254

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database :

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41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	75	10.0	80 6 AX204893	AX204893 Sequence
2	60	8.0	60 6 AX204894	AX204894 Sequence
3	60	8.0	60 6 AX204895	AX204895 Sequence
4	23	3.1	32 6 AX204942	AX204942 Sequence
5	21	2.8	21 6 AX024699	AX024699 Sequence
6	21	2.8	38 6 AX204943	AX204943 Sequence
7	20	2.7	20 6 AR042542	AR042542 Sequence
8	20	2.7	20 6 AX235033	AX235033 Sequence
9	20	2.7	29 6 AX024704	AX024704 Sequence
10	20	2.7	30 6 AX204905	AX204905 Sequence
11	20	2.7	31 6 AX204904	AX204904 Sequence
12	20	2.7	32 6 AR116917	AR116917 Sequence
13	20	2.7	32 6 AR159654	AR159654 Sequence
14	20	2.7	32 6 AR164509	AR164509 Sequence
15	20	2.7	32 6 AR182534	AR182534 Sequence
16	20	2.7	32 6 AX024702	AX024702 Sequence
17	20	2.7	32 6 AX079859	AX079859 Sequence
18	20	2.7	32 6 AX107125	AX107125 Sequence
19	20	2.7	32 6 AX235022	AX235022 Sequence
20	20	2.7	32 6 BD069517	BD069517 Isolated
21	19	2.5	19 6 AR042534	AR042534 Sequence
22	19	2.5	19 6 AR042539	AR042539 Sequence
23	19	2.5	19 6 AR144260	AR144260 Sequence
24	19	2.5	19 6 AR144262	AR144262 Sequence
25	19	2.5	19 6 AR209942	AR209942 Sequence
26	19	2.5	19 6 AR209944	AR209944 Sequence
27	19	2.5	19 6 AX235032	AX235032 Sequence
28	19	2.5	31 6 AR116916	AR116916 Sequence
29	19	2.5	31 6 AR159653	AR159653 Sequence
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31	19	2.5	31 6 AR182533	AR182533 Sequence
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35	19	2.5	31 6 BD069516	BD069516 Isolated
36	18	2.4	18 6 AR042538	AR042538 Sequence
37	18	2.4	18 6 AX235035	AX235035 Sequence
38	18	2.4	18 6 AX235036	AX235036 Sequence
39	18	2.4	21 6 AX696140	AX696140 Sequence
40	18	2.4	30 6 AX024703	AX024703 Sequence
41	17	2.3	17 6 AR042541	AR042541 Sequence
42	17	2.3	17 6 AR144261	AR144261 Sequence
43	17	2.3	17 6 AR209943	AR209943 Sequence
44	17	2.3	17 6 AX235031	AX235031 Sequence
45	17	2.3	17 6 AX422233	AX422233 Sequence

ALIGNMENTS

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LOCUS	AX204893	Sequence 24 from Patent WO0155393.				
DEFINITION	AX204893					
ACCESSION	AX204893					
KEYWORDS	AX204893.1 GI:15394218					
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS	1	Wang, R.F., Rosenberg, S.A. and Zeng, G.				
TITLE		MHC class II restricted T cell epitopes from the cancer antigen				
JOURNAL		NY-esc-1				
		Patent: WO 0155393-A 24 02-AUG-2001;				

FEATURES The Secretary, Department of Health and Human Services (US)

SOURCE

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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Artificial"
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Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 384 CAGATGCGCCACCGCTTCCCGTGCAGGGGTGCTTGAAGAGTTCATGTGTCGCGC 443
DB 1 CAGATGCGCCACCGCTTCCCGTGCAGGGGTGCTTGAAGAGTTCATGTGTCGCGC 60

QY 444 AACATCTGACTATC 458
DB 61 AACATCTGACTATC 75

RESULT 2
LOCUS AX204894 60 bp DNA linear PAT 30-AUG-2001

DEFINITION Sequence 25 from Patent WO0155393.
ACCESSION AX204894
VERSION AX204894.1 GI:15394219

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
ARTIFACTIAL sequences.

REFERENCE 1
AUTHORS Wang, R.F., Rosenberg, S.A. and Zeng, G.
TITLE MHC class II restricted T cell epitopes from the cancer antigen
NY-ESO-1

JOURNAL Patent: WO 0155393-A 25 02-AUG-2001;
The Secretary, Department of Health and Human Services (US)

FEATURES
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/note="Artificial"

BASE COUNT 11 a 24 c 10 g 15 t
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Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 473 AGACCAACCGCCACGCTCTCATGAGCTCCCTGTCAGAGGCTTCCCTGTGAT 532
DB 1 AGACCAACCGCCACGCTCTCATGAGCTCCCTGTCAGAGGCTTCCCTGTGAT 60

RESULT 3
LOCUS AX204895 60 bp DNA linear PAT 30-AUG-2001

DEFINITION Sequence 26 from Patent WO0155393.
ACCESSION AX204895
VERSION AX204895.1 GI:15394221

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
ARTIFACTIAL sequences.

REFERENCE 1
AUTHORS Wang, R.F., Rosenberg, S.A. and Zeng, G.
TITLE MHC class II restricted T cell epitopes from the cancer antigen
NY-ESO-1
JOURNAL Patent: WO 0155393-A 26 02-AUG-2001;
The Secretary, Department of Health and Human Services (US)

FEATURES Location/Qualifiers

SOURCE
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Best Local Similarity 100.0%; Pred. No. 1.3e-22;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 534 TGGATCAGCGAGTGTCTTCTGCCCGTGTGCTTGGCTCAGCCTCCTCAGGGCAGAGGCGC 593
DB 1 TGGATCAGCGAGTGTCTTCTGCCCGTGTGCTTGGCTCAGCCTCCTCAGGGCAGAGGCGC 60

RESULT 4
LOCUS AX204942 32 bp DNA linear PAT 30-AUG-2001

DEFINITION Sequence 73 from Patent WO0155393.
ACCESSION AX204942
VERSION AX204942.1 GI:15394226

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
ARTIFACTIAL sequences.

REFERENCE 1
AUTHORS Wang, R.F., Rosenberg, S.A. and Zeng, G.
TITLE MHC class II restricted T cell epitopes from the cancer antigen
NY-ESO-1

JOURNAL Patent: WO 0155393-A 73 02-AUG-2001;
The Secretary, Department of Health and Human Services (US)

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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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BASE COUNT 7 a 9 c 12 g 4 t
ORIGIN

Query Match 3.1%; Score 23; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 CATGACGCGCCGAGGCGCGGCA 75
DB 10 CATGACGCGCCGAGGCGCGGCA 32

RESULT 5
LOCUS AX024699/c 21 bp DNA linear PAT 15-SEP-2000

DEFINITION Sequence 15 from Patent EP1001022.
ACCESSION AX024699
VERSION AX024699.1 GI:10184783

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
ARTIFACTIAL sequences.

REFERENCE 1
AUTHORS Arnould, C.A. and Schrier, P.
TITLE Camel, an alternative translation product of the tumour antigen
lage-1
JOURNAL Patent: EP 1001022-A 15 17-MAY-2000;
BOEHRINGER INGELHEIM INT (DE); UNIV HOSPITAL LEIDEN (NL)

FEATURES
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1. .21
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/db_xref="taxon:32630"


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DEFINITION   Sequence 36 from Patent WO0155393.
ACCESSION    AX204905
VERSION      AX204905.1 GI:15394225
KEYWORDS     .
SOURCE       synthetic construct
ORGANISM     synthetic construct
              artificial sequences.
REFERENCE    1
AUTHORS      Wang, R.F., Rosenberg, S.A. and Zeng, G.
TITLE        MHC class II restricted T cell epitopes from the cancer antigen
              my-eso-1
JOURNAL      Patent: WO 0155393-A 36 02-AUG-2001;
              The Secretary, Department of Health and Human Services (US)
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Db 30 AGAGGCGCTAAGCCGAGCCT 11

RESULT 11
LOCUS       AX204904                31 bp    DNA        linear    PAT 30-AUG-2001
DEFINITION   Sequence 35 from Patent WO0155393.
ACCESSION    AX204904
VERSION      AX204904.1 GI:15394224
KEYWORDS     .
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    1
AUTHORS      Wang, R.F., Rosenberg, S.A. and Zeng, G.
TITLE        MHC class II restricted T cell epitopes from the cancer antigen
              my-eso-1
JOURNAL      Patent: WO 0155393-A 35 02-AUG-2001;
              The Secretary, Department of Health and Human Services (US)
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              /db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 ATGCAGGCCGAGAGCCGGGG 73
Db 12 ATGCAGGCCGAGAGCCGGGG 31

RESULT 12
LOCUS       AR116917/c              32 bp    DNA        linear    PAT 16-MAY-2001
DEFINITION   Sequence 10 from patent US 6140050.
ACCESSION    AR116917
VERSION      AR116917.1 GI:14097823
KEYWORDS     .

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SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 32)
AUTHORS      Sahin, U., Tureci, O., Chen, Y.-T., Old, L.J. and Pfreundschuh, M.
TITLE        Methods for determining breast cancer and melanoma by assaying for
              a plurality of antigens associated therewith
JOURNAL      Patent: US 6140050-A 10 31-OCT-2000;
              Location/Qualifiers
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BASE COUNT   6 a                12 c                7 g                7 t
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Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 580 CAGGGCAGAGCGCGCTAAGCC 599
Db 32 CAGGGCAGAGCGCGCTAAGCC 13

RESULT 13
LOCUS       AR159654/c              32 bp    DNA        linear    PAT 17-OCT-2001
DEFINITION   Sequence 3 from patent US 6251603.
ACCESSION    AR159654
VERSION      AR159654.1 GI:16222378
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 32)
AUTHORS      Jager, E., Stockert, E., Old, L.J. and Knuth, A.
TITLE        Method for determining status of a cancerous condition by
              determining antibodies to NY-ESO-1 in a patient sample
JOURNAL      Patent: US 6251603-A 3 26-JUN-2001;
              Location/Qualifiers
FEATURES     source
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              /organism="unknown"
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14
LOCUS       AR164509/c              32 bp    DNA        linear    PAT 17-OCT-2001
DEFINITION   Sequence 3 from patent US 6274145.
ACCESSION    AR164509
VERSION      AR164509.1 GI:16237561
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 32)
AUTHORS      Chen, Y.-T., Scanlan, M., Gure, A., Old, L.J., Jager, E., Alexander, K.,
              Drifflout, J.W., Tureci, O., Sahin, U. and Pfreundschuh, M.
TITLE        Isolated nucleic acid molecule encoding cancer associated antigen,
              the antigen itself, and uses thereof
JOURNAL      Patent: US 6274145-A 3 14-AUG-2001;
              Location/Qualifiers
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RESULT 15

ARI82534/c ARI82534 32 bp DNA linear PAT 20-APR-2002

LOCUS DEFINITION Sequence 10 from patent US 6338947.
 ARI82534
 ARI82534.1 GI:20225741

KEYWORDS
 SOURCE Unknown.

ORGANISM Unknown.
 Unclassified.

REFERENCE 1 (bases 1 to 32)
 AUTHORS Sahin, U., Tureci, O., Chen, Y.-T., Old, L.J. and Pfreundschuh, M.
 TITLE Methods for determining breast cancer and melanoma by assaying for
 a plurality of antigens associated therewith
 JOURNAL Patent: US 6338947-A 10 15 JAN-2002;
 FEATURES Location/Qualifiers

source

BASE COUNT 6 a 12 c 7 g 7 t
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Search completed: February 17, 2004, 19:33:24
 Job time : 3059 secs

Wed Feb 18 12:49:30 2004

us-10-023-182-1.oliszm.rng

Page 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 17, 2004, 17:03:58 ; Search time 299 Seconds

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6789.222 Million cell updates/sec

Title: US-10-023-182-1

Perfect score: 752
Sequence: 1 ATCCTCGTGGGCGCTGACCT.....TAAACGAGCTACGAAAA 752

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	10.0	80	22	AAD14181 Human NY ESO-1 MHC
2	60	8.0	60	22	AAD14182 Human NY ESO-1 MHC
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4	60	8.0	60	24	ABN35949 Human spliced tran
*5	30	4.0	30	20	AAK58600 Human cancer anti
6	30	4.0	30	20	AAK58601 Human cancer anti
7	27	3.6	20	20	AAK58602 Human cancer anti
8	25	3.3	51	22	AAK33471 Human SNP oligonuc

9	23	3.1	23	20	AAK58603 Human cancer anti
10	23	3.1	32	22	AAD14188 Human NY ESO-1 gen
c 11	22	2.9	22	20	AAK58604 Human cancer anti
c 12	21	2.8	21	21	AAD00156 Reverse PCR primer
c 13	21	2.8	38	22	AAD14189 Human NY ESO-1 gen
14	20	2.7	20	19	AAV50356 Human NY ESO-1 PCR p
15	20	2.7	20	22	AAH75127 PCR primer for can
16	20	2.7	29	21	AAD00161 PCR primer 48-A,
c 17	20	2.7	30	22	AAD14187 ESO-3p PCR primer
c 18	20	2.7	31	22	AAV38568 PCR primer used to
c 19	20	2.7	32	21	AAD00159 PCR primer for NY-
c 20	20	2.7	32	21	AAZ49179 Human tumour anti
c 21	20	2.7	32	21	AAZ38382 PCR primer for can
c 22	20	2.7	32	22	AAH75120 Human NY-ESO-1 PCR
c 23	20	2.7	32	22	AAK58636 Human NY-ESO-1 PCR
c 24	20	2.7	32	22	AAK502256 Human NY-ESO-1 RT-
c 25	20	2.7	32	25	ABY96458 Human cancer-testi
c 26	20	2.7	32	25	ABT14656 Human LAGE-1 PCR p
c 27	20	2.5	19	19	AAV50351 Human LAGE-1 PCR p
c 28	19	2.5	19	19	AAV50353 PCR primer for can
c 29	19	2.5	19	22	AAK42535 NY-ESO-1 antisense
c 30	19	2.5	19	22	AAK4255 PCR primer used to
c 31	19	2.5	31	21	AAZ49178 PCR primer for NY-
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c 43	18	2.4	18	22	AAD14185 Human AAGA SNP ana
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ALIGNMENTS

RESULT 1
ID AAD14181 standard; DNA; 80 BP.

AC AAD14181;

DT 06-NOV-2001 (first entry)

DE Human NY ESO-1 MHC class II restricted T cell epitope DNA #1.

XX Human: major histocompatibility complex; MHC; vaccine; metastasis;

KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;

KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;

KW tumour-specific humoral-mediated immunity; cancer; cytostatic;

OS Homo sapiens.

XX WO200155393-A2.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US02765.

XX 28-JAN-2000; 2000US-0179004.

XX 29-SEP-2000; 2000US-0237107.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang F, Rosenberg SA, Zeng G;

DR WPI; 2001-496851/54.
XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX
XX
PS Claim 22; Page 33; 134pp; English.
XX
XX The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or hapten and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is human
CC NY ESO-1 MHC class II restricted T cell epitope DNA.
XX
SQ Sequence 80 BP; 15 A; 26 C; 21 G; 18 T; 0 other;
Query Match 10.0%; Score 75; DB 22; Length 80;
Best Local Similarity 100.0%; Pred. No. 3.6e-26;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 384 CAGGATGCCCAACGCGCTCCGCTGCGAGGGGCTTCGAGAGGCTTCATGTCGCGC 443
DB 1 CAGGATGCCCAACGCGCTCCGCTGCGAGGGGCTTCGAGAGGCTTCATGTCGCGC 60
QY 444 AACATCTGACTATC 458
DB 61 AACATCTGACTATC 75
Db
RESULT 2
AADI4182 standard; DNA; 60 BP.
XX
AC AADI4182;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human NY ESO-1 MHC class II restricted T cell epitope DNA #2.
XX
XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
KM class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KM NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KM tumour-specific humoral-mediated immunity; cancer; cytostatic;
KM immunotherapy; ds.
XX
OS Homo sapiens.
XX
PN WO200155393-A2.
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US02765.
XX
PR 28-JAN-2000; 2000US-0179004.
XX
PR 29-SEP-2000; 2000US-0237107.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Wang R, Rosenberg SA, Zeng G;
XX
XX WPI; 2001-496851/54.
XX

XX
XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX
XX
PS Claim 22; Page 33; 134pp; English.
XX
XX The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any
CC given target antigen and/or hapten and to induce tumour-specific
CC humoral-mediated immunity against cancer. The present sequence is human
CC NY ESO-1 MHC class II restricted T cell epitope DNA.
XX
SQ Sequence 60 BP; 11 A; 24 C; 10 G; 15 T; 0 other;
Query Match 8.0%; Score 60; DB 22; Length 60;
Best Local Similarity 100.0%; Pred. No. 6.8e-19;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 473 AGACCAACCGCAACCTGAGCTCCATGAGCTCCGCTGCGAGAGCTTCCTGTTGAT 532
DB 1 AGACCAACCGCAACCTGAGCTCCATGAGCTCCGCTGCGAGAGCTTCCTGTTGAT 60
QY
Db
RESULT 3
AADI4183 standard; DNA; 60 BP.
XX
AC AADI4183;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human NY ESO-1 MHC class II restricted T cell epitope DNA #3.
XX
XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
KM class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KM NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KM tumour-specific humoral-mediated immunity; cancer; cytostatic;
KM immunotherapy; ds.
XX
OS Homo sapiens.
XX
PN WO200155393-A2.
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US02765.
XX
PR 28-JAN-2000; 2000US-0179004.
XX
PR 29-SEP-2000; 2000US-0237107.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Wang R, Rosenberg SA, Zeng G;
XX
XX WPI; 2001-496851/54.
XX
XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis -
XX

PS Claim 22; Page 33; 134pp; English

The invention relates to the identification and isolation of major histocompatibility (MHC) class II restricted T cell epitope (MHC-II epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner. In particular HLA-DR or HLA-DP restricted. The products of the gene are promising candidates for immunotherapeutic strategies for the prevention, treatment and diagnosis of patients with cancer. The cancer epitopes are useful as immunogen and vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T lymphocytes resulting in protection of the recipient from development of cancer and protection from metastasis, or by inhibiting the growth of cells expressing the NY-ESO-1 gene product. The cancer peptides are also useful as diagnostic agent to detect the presence of cancer, to enhance the generation of antibody and/or CD8+ T cell responses against any given target antigen and/or happen and to induce tumour-specific humoral-mediated immunity against cancer. The present sequence is human NY ESO-1 MHC class II restricted T cell epitope DNA.

Sequence 60 BP; 7 A; 19 C; 18 G; 16 T; 0 other.

Query Match	8.0%	Score 60;	DB 22;	Length 60;
Best Local Similarity	100.0%	Pred. No. 6.8e-19;		
Matches 60;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

534 TGATACGCGAGTGTCTTCTGCGCCGTCGTTTTGGCTCAGCCCTCCCTCAGGGCAGAGGCGC 593

Db 1 TGATACGCGAGTGTCTTCTGCGCCGTCGTTTTGGCTCAGCCCTCCCTCAGGGCAGAGGCGC 60

RESULT 4
ABN35949
ID ABN35949 standard; DNA; 60 BP.

AC ABN359497

DT 15-JUL-2002 (first entry)

DE Human spliced detection oligonucleotide SEQ ID NO:8697.

KM Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.

05 Homo sapiens.

PN WO200210449-A2

PD 07-FEB-2002.

PF 20-JUL-2001; 2001WO-IB01903

PR 28-JUL-2000; 2000US-221607P

CONFIDENTIAL

XX
XX
DT

XX
DB WBT: 2002-257393/30

XX	DT	New of peptide
----	----	----------------

PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes -

PS Example 1; SEQ ID 8697; 47pp; English

CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcript units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridizing selectively to a

CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. AHN27253 to AHN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at http://wipo.int/pubdb/published_pat_sequences.

CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

Sequence 60 BP; 6 A; 18 C; 14 G; 22 T; 0 other;

Query Match	100.0%	Score 60;	DB 24;	Length 60;
Best Local Similarity	100.0%	Pred. No. 6-8e-19;		
Matches	60;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

Qy 505 CCGTCTCCAGCAGCTTTCCCTGTTGATGGATACGCAGCGCTTTCTGCCCGTGTTTT 564
Db 1 CCGTCTCCAGCAGCTTTCCCTGTTGATGGATACGCAGCGCTTTCTGCCCGTGTTTT 60			

RESULT 5	
AAx58600	
ID	AAx58600 standard; DNA; 30 BP

AC AAX58600;

DT 16-AUG-1999 (first entry)

DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide DNA

KM NY ESO-1/CAG-3 gene; cancer peptide; antigen; human;
 KM leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer

uterine cancer

KW Liver cancer

22

OS Synthetic.

PN WO9918206-A2.

PD 15-APR-1999.
XX

21-SEP-1998; 98MO-US19609.

PR 08-OCT-1997 3/05-006
XX

XX
FA / US DEPT HEALTH

[illegible]

DR P-PSDB; AAY05969.

PT Cancer antigen NY ESO1/CAG-3

PS Disclosure; Page 21, 88pp; English.
 XX
 CC This DNA sequence encodes a cancer peptide (see AA05969) based on
 CC amino acid residues 55-62 of human ESO-1/CAG-3 (or CAG-3) ORF1

(see AAY05965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their variants (see AAY05967-87), are useful as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancer such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent return to a patient. A recombinant virus comprising a nucleic acid sequence of the present sequence is claimed and is used in a claimed method of preventing or inhibiting cancer.

Sequence 30 BP; 2 A; 11 C; 16 G; 1 T; 0 other;

Query Match 4.0%; Score 30; DB 20; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

211 CCTGGGGGCGGAGGAGGCGGCGGCGGCGG 240
Db 1 CCTGGGGGCGGAGGAGGCGGCGGCGGCGG 30

RESULT 6
AAX58601
ID AAX58601 standard; DNA; 30 BP.

AC AAX58601;

DT 16-AUG-1999 (first entry)

DE Human cancer antigen NY ESO-1/CAG-3 ORF2 cancer peptide DNA.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KM leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KM metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KM uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KM cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KM liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KM vaccine; ss.

XX Homo sapiens.
OS Synthetic.

XX WO9918206-A2.

XX 15-APR-1999.

XX 21-SEP-1998; 98WO-US19609.

XX 08-OCT-1997; 97US-0061428.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Rosenberg SA, Wang RF;

XX WPI, 1999-277270/23.

XX P-PSDB; AAY05982.

XX Cancer antigen NY ESO1/CAG-3

XX Disclosure; Page 21; 88BP; English.

This DNA sequence encodes a cancer peptide (see AAY05982) based on amino acid residues 19-27 of human ESO-1/CAG-2 (or CAG-3) ORF2 (see AAY05966), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF2, CAG-3 ORF1 (see AAY05965), portions of them and their variants (see AAY05967-87), are useful as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide or tumour antigen; antibodies reacting with a CAG-3 cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancer such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent return to a patient. A recombinant virus comprising a nucleic acid sequence of the present sequence is claimed and is used in a claimed method of preventing or inhibiting cancer.

Sequence 30 BP; 4 A; 9 C; 15 G; 2 T; 0 other;

Query Match 4.0%; Score 30; DB 20; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

145 CTGGGGGCGGAGGAGGCGGCGGCGGCGG 174
Db 1 CTGGGGGCGGAGGAGGCGGCGGCGGCGG 30

RESULT 7
AAX58602
ID AAX58602 standard; DNA; 27 BP.

AC AAX58602;

DT 16-AUG-1999 (first entry)

DE Human cancer antigen NY ESO-1/CAG-3 ORF2 cancer peptide DNA.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KM leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KM metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KM uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KM cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KM liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KM vaccine; ss.

XX Homo sapiens.
OS Synthetic.

XX WO9918206-A2.

XX 15-APR-1999.

XX 21-SEP-1998; 98WO-US19609.

XX 08-OCT-1997; 97US-0061428.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Rosenberg SA, Wang RF;

XX WPI, 1999-277270/23.

XX P-PSDB; AAY05961.

XX Cancer antigen NY ESO1/CAG-3

PS Disclosure, Page 21, 88pp; English.

CC This DNA sequence encodes a cancer peptide (see AY05981) based on
 CC amino acid residues 20-27 of human ESO-1/CAG-2 (or CAG-3) ORF2
 CC (see AY05966), a new and potent tumour antigen capable of eliciting
 CC an antigen specific immune response by T cells. Cancer peptides
 CC derived from CAG-3 ORF2, CAG-3 ORF1 (see AY05965), portions of them
 CC and their variants (see AY05967-87), are useful as cancer vaccines
 CC that protect against cancer. The invention provides: vectors and
 CC host cells (also useful as vaccines); a method of diagnosis of
 CC cancer or precancer; a transgenic animal; antisense oligonucleotides
 CC that inhibit expression of the cancer peptide or tumour antigen;
 CC antibodies reacting with a CAG-3 cancer peptide, useful in
 CC diagnostic and detection assays; and methods for preventing or
 CC inhibiting cancer by administering a cancer peptide, with or without
 CC an HLA molecule. The cancer peptides form part of, or are derived
 CC from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer and
 CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
 CC thyroid cancers. Melanoma is treated by inducing cancer-specific T
 CC cells in vitro for subsequent return to a patient. A recombinant
 CC virus comprising a nucleic acid sequence of the present sequence
 CC is claimed and is used in a claimed method of preventing or
 CC inhibiting cancer.

CC Sequence 27 BP; 4 A; 8 C; 14 G; 1 T; 0 other;

SO Query Match 3.6%; Score 27; DB 20; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.0067;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 148 GCGGCCGAGAGAGCGGTCACAGG 174
 1 GCGGCCGAGAGAGCGGTCACAGG 27

Db

RESULT 8
 AAL33471
 ID AAL33471 standard; DNA; 51 BP.
 AC AAL33471;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Human SNP oligonucleotide #6679.
 XX
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
 KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200147944-A2.
 XX
 PD 05-JUL-2001.
 XX
 PF 28-DEC-2000; 2000WO-US35498.
 XX
 PR 28-DEC-1999; 98US-0173419.
 XX
 PR 27-DEC-2000; 2000US-0173419.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI *Shinkets RA, Leach M;
 XX
 DR WPI, 2001-465210/50.
 XX

PT Polymorphic nucleic acids encoding e.g. amyloses, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -

PS Claim 1; Page 3289; 4143pp; English.

CC The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amyloses, amyloid proteins, angiopoietin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histone, kinesin, colony stimulating factors, complement related
 CC proteins, cytochromes, kinases, cytokines, interleukins, interferons,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.

CC Sequence 51 BP; 10 A; 14 C; 22 G; 5 T; 0 other;

SO Query Match 3.3%; Score 25; DB 22; Length 51;
 Best Local Similarity 100.0%; Pred. No. 0.061;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 45 TCCGAGCCATGACAGCCGAGAGCC 69
 1 TCCGAGCCATGACAGCCGAGAGCC 25

Db

RESULT 9
 AAX58603
 ID AAX58603 standard; DNA; 23 BP.
 AC AAX58603;
 XX
 DT 16-AUG-1999 (first entry)
 XX
 DE Human cancer antigen NY ESO-1/CAG-3 primer ESO-P2.
 XX
 KW NY ESO-1/CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine; PCR; primer; ss.
 XX
 OS Synthetic.
 XX
 FN Homo sapiens.
 XX
 PD WO9918206-A2.
 XX
 PF 15-APR-1999.
 XX
 PF 21-SEP-1998; 98WO-US19609.
 XX
 PR 08-OCT-1997; 97US-0061428.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Rosenberg SA, Wang RF;
 XX
 DR WPI, 1999-277270/23.
 XX
 PT Cancer antigen NY ESO1/CAG-3
 XX
 PS Example 1, Page 32; 88pp; English.
 XX

CC Primer ESO-P2 and primer ESO-P5 (see AAX58604) were used in the
 CC PCR amplification of human ESO-1/CAG-2 cDNA sequences obtained from
 CC total RNA extracted from tumour cell lines. Cancer peptides
 CC derived from CAG-3, portions of them and their variants (see
 CC AAY05965-87), are useful as cancer vaccines that protect against
 CC cancer. The cancer peptides form part of, or are derived
 CC from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer and
 CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
 CC thyroid cancers.

SO Sequence 23 BP; 4 A; 4 C; 10 G; 5 T; 0 other;

Query Match 3.1%; Score 23; DB 20; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.58; Indels 0; Gaps 0;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 GCGGCTTCAGGCTGATGATG 277
 1 GCGGCTTCAGGCTGATGATG 23

RESULT 10
 AAD14188
 ID AAD14188 standard; DNA; 32 BP.
 XX AAD14188;
 AC
 XX 06-NOV-2001 (first entry)
 DT
 XX Human NY ESO-1 gene amplifying forward PCR primer.
 DE
 XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
 XX class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 XX NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
 XX tumour-specific humoral-mediated immunity; cancer; cytostatic;
 XX immunotherapy; PCR primer; ss.
 KM
 XX Homo sapiens.
 OS
 XX WO200155393-A2.
 XX
 XX 02-AUG-2001.
 PD
 XX 26-JAN-2001; 2001WO-US02765.
 XX PF
 XX 28-JAN-2000; 2000US-0179004.
 XX PR
 XX 29-SEP-2000; 2000US-0237107.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Wang R, Rosenberg SA, Zeng G;
 PI WPI; 2001-496851/54.
 XX
 XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 PT protection from metastasis
 XX
 XX Example 8; Page 50; 134pp; English.

CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 CC useful as diagnostic agent to detect the presence of cancer, to enhance
 CC the generation of antibody and/or CD8+ T cell responses against any
 CC given target antigen and/or hapten and to induce tumour-specific
 CC humoral-mediated immunity against cancer. The present sequence is
 CC forward PCR primer used to amplify human NY ESO-1 gene.

SO Sequence 32 BP; 7 A; 9 C; 12 G; 4 T; 0 other;

Query Match 3.1%; Score 23; DB 22; Length 32;
 Best Local Similarity 100.0%; Pred. No. 0.58; Indels 0; Gaps 0;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 CATGAGCGCGAGCGCGGCA 75
 10 CATGAGCGCGAGCGCGGCA 32

RESULT 11
 AAX58604/C
 ID AAX58604 standard; DNA; 22 BP.
 XX AAX58604;
 AC
 XX 16-AUG-1999 (first entry)
 DT
 XX Human cancer antigen NY ESO-1/CAG-3 primer ESO-P5.
 DE
 XX NY ESO-1/CAG-3 gene; cancer peptide; antigen; human;
 XX leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 XX metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 XX uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 XX cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 XX liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 XX vaccine; PCR; primer; ss.
 KM
 XX Synthetic.
 OS
 XX Homo sapiens.
 XX
 XX WO9918206-A2.
 XX
 XX 15-APR-1999.
 PD
 XX 21-SEP-1998; 98WO-US19609.
 XX PF
 XX 08-OCT-1997; 97US-0061428.
 XX PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Rosenberg SA, Wang RF;
 PI WPI; 1999-277270/23.
 XX
 XX Cancer antigen NY ESO1/CAG-3
 PT
 XX Example 1; Page 32; 88pp; English.

CC Primer ESO-P5 and primer ESO-P2 (see AAX58603) were used in the
 CC PCR amplification of human ESO-1/CAG-2 cDNA sequences obtained from
 CC total RNA extracted from tumour cell lines. Cancer peptides
 CC derived from CAG-3, portions of them and their variants (see
 CC AAY05965-87), are useful as cancer vaccines that protect against
 CC cancer. The cancer peptides form part of, or are derived
 CC from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer and
 CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
 CC thyroid cancers.

SO Sequence 22 BP; 5 A; 10 C; 4 G; 3 T; 0 other;

Query Match 2.9%; Score 22; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.8;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 689 TGTGCTGGAGAGAGCGCTT 710
 |||||
 DB 22 TGTGCTGGAGAGAGCGCTT 1

RESULT 12
 AAD00156/C
 ID AAD00156 standard; DNA; 21 BP.
 XX
 AC AAD00156;
 XX
 DT 31-JUL-2000 (first entry)
 XX
 DE Reverse PCR primer R2, for construction of pCR-464 vector.
 XX
 XX CAMEL; CTL-recognised Antigen on Melanoma; cytotoxic T lymphocyte; CTL;
 KW tumour-associated antigen; LAGE-1; NY-ESO-1; anticancer; melanoma; human;
 KW cancer; immunotherapy; immune response; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200023584-A1.
 XX
 PD 27-APR-2000.
 XX
 PF 15-OCT-1999; 99WO-EP07832.
 XX
 PR 16-OCT-1998; 98EP-0119583.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 PA (UYHO-) UNIV HOSPITAL LEIDEN.
 XX
 PI Schrier PI, Aarnoudse CA, Heider K, Klade C;
 DR WPI; 2000-339685/29.
 XX
 PI Tumor-associated antigen useful for cancer immunotherapy is encoded by
 PT the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA -
 XX
 PS Disclosure; Page 66; 73pp; English.
 XX
 CC The present DNA sequence is the reverse PCR primer R2, used along with
 CC forward PCR primer SP6F-PSV, to generate the deletion construct.
 CC PCR-464 of CAMEL cDNA clone 4H8.
 CC The tumour-associated antigen, CAMEL (Cytotoxic T lymphocytes (CTL)-
 CC recognised Antigen on Melanoma) is encoded by the open reading frame
 CC (ORF)-1 of LAGE-1 gene, a tumour-specific antigen. It shows strong
 CC homology with NY-ESO-1, a tumour-specific antigen. The tumour-associated
 CC antigen displayed on melanoma cells is recognised by cytotoxic T
 CC lymphocytes. CAMEL is expressed in tumour cell lines, tumour tissues
 CC (e.g. breast and lung) and in restricted number of healthy tissues. It
 CC has anticancer activity. CAMEL tumour antigen and immunogenic peptides
 CC derived from it are useful for cancer immunotherapy. They have the
 CC potential to induce an immune response, by eliciting a CTL response. The
 CC DNA molecule is used for construction of recombinant or fusion proteins.
 XX
 SQ Sequence 21 BP; 6 A; 7 C; 4 G; 4 T; 0 other;

Query Match 2.8%; Score 21; DB 21; Length 21;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 528 TTGATGTGATCAGCAGTGC 548
 |||||
 DB 21 TTGATGTGATCAGCAGTGC 1

RESULT 13
 AAD14189/C
 ID AAD14189 standard; DNA; 38 BP.
 XX

AC AAD14189;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human NY ESO-1 gene amplifying reverse PCR primer.
 XX
 KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
 KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
 KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
 KW immunotherapy; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200155393-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 26-JAN-2001; 2001WO-US02765.
 XX
 PR 28-JAN-2000; 2000US-0179004.
 XX
 PR 29-SEP-2000; 2000US-0237107.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Wang R, Rosenberg SA, Zeng G;
 DR WPI; 2001-496851/54.
 XX
 PI New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 PT protection from metastasis -
 XX
 PS Example 8; Page 50; 134pp; English.
 XX
 CC The invention relates to the identification and isolation of major
 CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
 CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 CC restricted. The products of the gene are promising candidates for
 CC immunotherapeutic strategies for the prevention, treatment and diagnosis
 CC of patients with cancer. The cancer epitopes are useful as immunogen and
 CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 CC lymphocytes resulting in protection of the recipient from development of
 CC cancer and protection from metastasis, or by inhibiting the growth of
 CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 CC useful as diagnostic agent to detect the presence of cancer, to enhance
 CC the generation of antibody and/or CD8+ T cell responses against any
 CC given target antigen and/or happen and to induce tumour-specific
 CC humoral-mediated immunity against cancer. The present sequence is
 CC reverse PCR primer used to amplify human NY ESO-1 gene.
 XX
 SQ Sequence 38 BP; 6 A; 13 C; 11 G; 8 T; 0 other;

Query Match 2.8%; Score 21; DB 22; Length 38;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 578 CTCAGGCGCAGAGCGCTAAGC 598
 |||||
 DB 38 CTCAGGCGCAGAGCGCTAAGC 18

RESULT 14
 AAV50356
 ID AAV50356 standard; cDNA; 20 BP.
 XX
 AC AAV50356;
 XX
 DT 27-OCT-1998 (first entry)
 XX
 DE Human LAGE-1 PCR primer BLE74.

```

XX Human; LAGE-1; tumour associated protein; IL-1; diagnosis; tumour;
KM PCR primer; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9832855-A1.
XX
XX 30-JUL-1998.
XX
XX 27-JAN-1998; 98WO-US01445.
XX
XX 27-JAN-1997; 97US-0791495.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Boon-Falleur T, De Smet C, Godelaine D, Leche B;
XX Lucas S;
XX
XX WPI; 1998-427951/36.
XX
XX New isolated LAGE-1 tumour associated nucleic acids - used to
XX develop products for the diagnosis and treatment of LAGE-1
XX associated disorders, particularly tumours
XX
XX Disclosure; Page 60; 73pp; English.
XX
XX The present sequence represents a PCR primer for LAGE-1 tumour
XX associated protein (TAP). The present invention also describes: (1) a
XX method for treating a subject with a disorder characterised by
XX expression of a LAGE-1 nucleic acid molecule or an expression product,
XX comprising administering to the subject autologous cytolytic T cells to
XX ameliorate the disorder, where the cytolytic T cells are specific for
XX complexes of an HLA molecule and a LAGE-1 TAP or an immunogenic
XX fragment; (2) a method for treating a subject with a disorder
XX characterised by expression of a LAGE-1 nucleic acid molecule or an
XX expression product, comprising administering a LAGE-1 TAP or an
XX immunogenic fragment to ameliorate the disorder; and (3) a method for
XX selectively enriching a population of T cells with cytolytic T cells
XX specific for a LAGE-1 TAP comprising contacting an isolated population
XX of T cells with an agent presenting a complex of a LAGE TAP or an
XX immunogenic fragment and a HLA presenting molecule to selectively
XX enrich the isolated population of T cells with the cytolytic T cells.
XX The methods and products from the present invention can be used for the
XX diagnosis and treatment of LAGE-1 associated disorders, particularly
XX tumours.
XX
XX Sequence 20 BP; 5 A; 3 C; 8 G; 4 T; 0 other;
XX
XX Query Match 2.7%; Score 20; DB 19; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 17;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 265 GGCTGAATGATGCTGCAGA 284
XX 1 GGCTGAATGATGCTGCAGA 20
XX
XX Db
XX
XX RESULT 15
XX AAH75127
XX ID AAH75127 standard; DNA; 20 BP.
XX
XX AAH75127;
XX
XX 13-NOV-2001 (first entry)
XX
XX PCR primer for cancer testis tumour antigen NY-ESO-1 DNA.
XX
XX Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
XX HLA; HLA binding peptide; major histocompatibility complex; MHC;
XX tumour; cancer; testis tumour; PCR primer; ss.
XX

```

```

XX Homo sapiens.
XX
XX WO200162917-A1.
XX
XX 30-AUG-2001.
XX
XX 22-JAN-2001; 2001WO-US02126.
XX
XX 22-FEB-2000; 2000US-0510635.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Leche B, Boon-Falleur T;
XX
XX WPI; 2001-550091/61.
XX
XX Genomic sequences of tumour associated antigen Ey-ESO-1 (LAGE-2) useful
XX for diagnosing testicular tumours -
XX
XX Example 15; Page 46; 50pp; English.
XX
XX The present PCR primer was used to amplify DNA encoding cancer
XX testis tumour antigen NY-ESO-1 (also called LAGE-2). NY-ESO-1 is a
XX molecule that is processed to at least one human leukocyte antigen
XX (HLA) binding peptide, which binds to Class I and Class II major
XX histocompatibility complex (MHC). NY-ESO-1 is expressed in tumour
XX mRNA and in testis, but not normal colon, kidney, liver or brain
XX tissue. The presence or level of expression of NY-ESO-1 may be assayed
XX for the diagnosis of cancer, especially testis tumours.
XX
XX Sequence 20 BP; 5 A; 3 C; 8 G; 4 T; 0 other;
XX
XX Query Match 2.7%; Score 20; DB 22; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 17;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 265 GGCTGAATGATGCTGCAGA 284
XX 1 GGCTGAATGATGCTGCAGA 20
XX
XX Db
XX
XX Search completed: February 17, 2004, 18:42:11
XX Job time : 301 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 17, 2004, 18:14:34 ; Search time 73 Seconds
(without alignments)
4546.851 Million cell updates/sec

Title: US-10-023-182-1

Perfect score: 752

Sequence: 1 ATCTCTGCGGCGCTGACCT.....TAAACTGAGCTACGAAAA 752

Scoring table: OLIGO NUC

Searched: 569978 seqs, 220691566 residues

Word size: 0

Total number of hits satisfying chosen parameters: 830498

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database: Issued Patents NA.*

1: /cgm2_6/ptodata/2/ina/5A.COMB.seq.*
2: /cgm2_6/ptodata/2/ina/5B.COMB.seq.*
3: /cgm2_6/ptodata/2/ina/6A.COMB.seq.*
4: /cgm2_6/ptodata/2/ina/6B.COMB.seq.*
5: /cgm2_6/ptodata/2/ina/6C.COMB.seq.*
6: /cgm2_6/ptodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2.7	2.7	20	1	US-08-791-495-14
2	2.7	2.7	20	1	US-08-791-495-14
3	2.7	2.7	20	1	US-08-791-495-14
4	2.7	2.7	20	1	US-08-791-495-14
5	2.7	2.7	20	1	US-08-791-495-14
6	2.7	2.7	20	1	US-08-791-495-14
7	2.7	2.7	20	1	US-08-791-495-14
8	2.7	2.7	20	1	US-08-791-495-14
9	2.7	2.7	20	1	US-08-791-495-14
10	2.7	2.7	20	1	US-08-791-495-14
11	2.7	2.7	20	1	US-08-791-495-14
12	2.7	2.7	20	1	US-08-791-495-14
13	2.7	2.7	20	1	US-08-791-495-14
14	2.7	2.7	20	1	US-08-791-495-14
15	2.7	2.7	20	1	US-08-791-495-14
16	2.7	2.7	20	1	US-08-791-495-14
17	2.7	2.7	20	1	US-08-791-495-14
18	2.7	2.7	20	1	US-08-791-495-14
19	2.7	2.7	20	1	US-08-791-495-14
20	2.7	2.7	20	1	US-08-791-495-14
21	2.7	2.7	20	1	US-08-791-495-14
22	2.7	2.7	20	1	US-08-791-495-14
23	2.7	2.7	20	1	US-08-791-495-14
24	2.7	2.7	20	1	US-08-791-495-14
25	2.7	2.7	20	1	US-08-791-495-14
26	2.7	2.7	20	1	US-08-791-495-14
27	2.7	2.7	20	1	US-08-791-495-14

C 28	15	2.0	26	2	US-09-003-067-72	Sequence 72, Appl
C 29	15	2.0	30	2	US-08-174-672D-76	Sequence 76, Appl
C 30	15	2.0	30	2	US-08-174-672D-97	Sequence 97, Appl
C 31	15	2.0	30	2	US-08-174-672D-98	Sequence 98, Appl
C 32	15	2.0	38	1	US-08-183-214-5	Sequence 5, Appl
C 33	15	2.0	42	3	US-08-874-825-6	Sequence 6, Appl
C 34	15	2.0	42	3	US-08-663-824-6	Sequence 6, Appl
C 35	15	2.0	42	3	US-09-231-303-6	Sequence 6, Appl
C 36	15	2.0	47	4	US-09-641-638-914	Sequence 914, App
C 37	15	2.0	48	3	US-08-874-825-5	Sequence 5, Appl
C 38	15	2.0	48	3	US-08-663-824-5	Sequence 5, Appl
C 39	15	2.0	48	4	US-09-231-303-5	Sequence 5, Appl
C 40	15	2.0	57	1	US-08-642-255-21	Sequence 21, Appl
C 41	15	2.0	57	2	US-08-290-731C-8	Sequence 8, Appl
C 42	14	1.9	20	1	US-08-255-561-9	Sequence 9, Appl
C 43	14	1.9	20	1	US-08-594-600-9	Sequence 9, Appl
C 44	14	1.9	20	4	US-09-844-634-112	Sequence 112, App
C 45	14	1.9	21	4	US-09-462-975-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-791-495-14
Patent No 5811519
GENERAL INFORMATION:
APPLICANT: Leth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
TITLE OF INVENTION: L1-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Wolf, Greenfield & Sacke, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-791-495-14
Query Match 2.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 GGCTGAATGATGCTGCAGA 284

Db 1 GGCTGAATGATGCTGCAGA 20

RESULT 2

US-09-105-907-10/c
Sequence 10, Application US/09105907A
Patent No. 6140050
GENERAL INFORMATION:
APPLICANT: Sahin, Ugur
APPLICANT: Tureci, Ozlem
APPLICANT: Chen, Yao-Tseng
APPLICANT: Old, Lloyd
APPLICANT: Pfrendachuh, Michael
TITLE OF INVENTION: Methods for Determining Breast Cancer And Melanoma By Assaying
TITLE OF INVENTION: For A Plurality of Antigens Associated Therewith
FILE REFERENCE: LUD 5544
CURRENT APPLICATION NUMBER: US/09/105,907A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 10
LENGTH: 32
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-105-907-10

Query Match 2.7%; Score 20; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 580 CAGGCGAGAGCGGCTAGACC 599

Db 32 CAGGCGAGAGCGGCTAGACC 13

RESULT 3

US-09-359-503-3/c
Sequence 3, Application US/09359503
Patent No. 6251603
GENERAL INFORMATION:
APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
APPLICANT: Knuth, Alexander
TITLE OF INVENTION: Method for Determining Status of A
TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
TITLE OF INVENTION: a Patient Sample
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,503
FILING DATE: July 23, 1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/165,546
FILING DATE: October 2, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
PRIOR APPLICATION DATA:

to NY-

APPLICATION NUMBER: 08/937,263

FILING DATE: September 15, 1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/752,182

FILING DATE: 03-October-1996

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6251603man, D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5466.1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 318-3000

TELEFAX: (212) 752-8958

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-359-503-3

Query Match 2.7%; Score 20; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 580 CAGGCGAGAGCGGCTAGACC 599

Db 32 CAGGCGAGAGCGGCTAGACC 13

RESULT 4

US-09-062-422-3/c
Sequence 3, Application US/09062422
Patent No. 6252052
GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew; Knuth, Alexander;
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: ANTIBODIES WHICH BIND TO NY-ESO-1
TITLE OF INVENTION: CANCER ASSOCIATED PROTEINS, USES THEREOF, TRUNCATED
TITLE OF INVENTION: FORMS OF NY-ESO-1, AND HLA BINDING PEPTIDES DERIVED
TITLE OF INVENTION: THEREFROM
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,422
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6252052man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-062-422-3

Query Match 2.7%; Score 20; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 580 CAGGGCAGAGCGGCTTAAGCC 599
DB 32 CAGGGCAGAGCGGCTTAAGCC 13

RESULT 5
US-08-937-263B-3/C

Sequence 3, Application US/08937263B
Patent No. 6274145

GENERAL INFORMATION:

APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;

APPLICANT: Alexander, Knuth; Drifflough, Jan W.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE

TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
TITLE OF INVENTION: ITSELF, AND USES THEREOF

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESS: Fulbright & Jaworski, L.L.P.

STREET: 666 Fifth Avenue
CITY: New York City

STATE: New York
COUNTRY: USA

ZIP: 10103

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

COMPUTER: IBM
OPERATING SYSTEM: PC-DOS

SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/937,263B
FILING DATE: September 15, 1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182

FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:

NAME: Sinn, Eric, Patent Agent
REGISTRATION NUMBER: 40,177

REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 32 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

US-08-937-263B-3

Query Match 2.7%; Score 20; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 580 CAGGGCAGAGCGGCTTAAGCC 599
DB 32 CAGGGCAGAGCGGCTTAAGCC 13

RESULT 6
US-09-578-378-10/C
Sequence 10, Application US/09578378
Patent No. 6338947

GENERAL INFORMATION:

APPLICANT: Sahin, Ugur
APPLICANT: Tureci, Ozlem

APPLICANT: Chen, Yao-Tseng
APPLICANT: Old, Lloyd

APPLICANT: Pfundschnub, Michael
TITLE OF INVENTION: Methods for Determining Breast Cancer And Melanoma By Assaying

TITLE OF INVENTION: Methods For Determining Breast Cancer And Melanoma By Assaying
FILE REFERENCE: LUD 5544

CURRENT FILING DATE: 2000-05-25
CURRENT APPLICATION NUMBER: US/09/578,378

PRIOR FILING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26

NUMBER OF SEQ ID NOS: 18
SEQ ID NO 10

LENGTH: 32
TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:

US-09-578-378-10

Query Match 2.7%; Score 20; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 580 CAGGGCAGAGCGGCTTAAGCC 599
DB 32 CAGGGCAGAGCGGCTTAAGCC 13

RESULT 7
US-09-751-798-3/C

Sequence 3, Application US/09751798
Patent No. 6525177

GENERAL INFORMATION:

APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;

APPLICANT: Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer

TITLE OF INVENTION: Associated Proteins, Uses Thereof,
TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESS: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue

CITY: New York City
STATE: New York

COUNTRY: USA
ZIP: 10103

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

COMPUTER: IBM
OPERATING SYSTEM: PC-DOS

SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/751,798
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422

FILING DATE:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6525177man D.

REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168

TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-751-798-3

Query Match 2.7%; Score 20; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 580 CAGGCGAGAGCGCTAGCC 599
Db 32 CAGGCGAGAGCGCTAGCC 13

RESULT 8
US-08-791-495-3/c
Sequence 3, Application US/08791495
Patent No. 5811519
GENERAL INFORMATION:
APPLICANT: Leth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: IL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-791-495-3

Query Match 2.5%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 521 TTCCTGTGATGTGATC 539
Db 19 TTCCTGTGATGTGATC 1

RESULT 9

US-08-791-495-11/c
Sequence 11, Application US/08791495
Patent No. 5811519
GENERAL INFORMATION:
APPLICANT: Leth, Bernard
APPLICANT: Lucas, Sophie
APPLICANT: De Smet, Charles
APPLICANT: Godelaine, Daniele
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: IL-1 TUMOR SPECIFIC GENES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,495
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-791-495-11

Query Match 2.5%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 647 TCCAGCAGAGTGGCCAG 665
Db 19 TCCAGCAGAGTGGCCAG 1

RESULT 10
US-09-183-931-22/c
Sequence 22, Application US/09183931C
Patent No. 6210886
GENERAL INFORMATION:
APPLICANT: Van Baren, Nicolas
APPLICANT: Brasseur, Francis
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
FILE REFERENCE: LUD 5527.1-JEL/ES
CURRENT APPLICATION NUMBER: US/09/183,931C
CURRENT FILING DATE: 2000-02-28
EARLIER APPLICATION NUMBER: US 09/018,422
EARLIER FILING DATE: 1998 - 02 - 04
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 22

```

; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: PCR primer
; OTHER INFORMATION: Synthesized by oligonucleotide synthesis machine
US-09-183-931-22

Query Match          2.5%; Score 19; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 647 TCCGACGACGAGTGCCGAG 665
Db 19 TCCGACGACGAGTGCCGAG 1

RESULT 11
US-09-183-931-24/C
; Sequence 24, Application US/09183931C
; Patent No. 6210886
; GENERAL INFORMATION:
; APPLICANT: Van Baren, Nicolas
; APPLICANT: Brasseur, Francis
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
; FILE REFERENCE: LUD 5527.1-JEL/ES
; CURRENT APPLICATION NUMBER: US/09/183,931C
; PRIOR FILING DATE: 2000-02-28
; EARLIER FILING DATE: 1998 - 02 - 04
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: PCR primer
; OTHER INFORMATION: Synthesized by oligonucleotide synthesis machine
US-09-183-931-24

Query Match          2.5%; Score 19; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 647 TCCGACGACGAGTGCCGAG 665
Db 19 TCCGACGACGAGTGCCGAG 1

RESULT 12
US-09-705-160-22/C
; Sequence 22, Application US/09705160
; Patent No. 6387630
; GENERAL INFORMATION:
; APPLICANT: Van Baren, Nicolas
; APPLICANT: Brasseur, Francis
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
; FILE REFERENCE: LUD 5527.3-JEL/MAS
; CURRENT APPLICATION NUMBER: US/09/705,160
; PRIOR FILING DATE: 2001-11-02
; PRIOR FILING DATE: 1998 - 10 - 30
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 22
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE: PCR primer
; OTHER INFORMATION: Synthesized by oligonucleotide synthesis machine
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US-09-705-160-22

Query Match          2.5%; Score 19; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 647 TCCGACGACGAGTGCCGAG 665
Db 19 TCCGACGACGAGTGCCGAG 1

RESULT 13
US-09-705-160-24/C
; Sequence 24, Application US/09705160
; Patent No. 6387630
; GENERAL INFORMATION:
; APPLICANT: Van Baren, Nicolas
; APPLICANT: Brasseur, Francis
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
; FILE REFERENCE: LUD 5527.3-JEL/MAS
; CURRENT APPLICATION NUMBER: US/09/705,160
; PRIOR FILING DATE: 2001-11-02
; PRIOR FILING DATE: 1998 - 10 - 30
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE: PCR primer
; OTHER INFORMATION: Synthesized by oligonucleotide synthesis machine
US-09-705-160-24

Query Match          2.5%; Score 19; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 647 TCCGACGACGAGTGCCGAG 665
Db 19 TCCGACGACGAGTGCCGAG 1

RESULT 14
US-09-105-907-9
; Sequence 9, Application US/09105907A
; Patent No. 6140050
; GENERAL INFORMATION:
; APPLICANT: Sahin, Ugur
; APPLICANT: Tureci, Ozlem
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; APPLICANT: Pfrendschuh, Michael
; TITLE OF INVENTION: Methods For Determining Breast Cancer And Melanoma By Assaying
; FILE REFERENCE: LUD 5544
; CURRENT APPLICATION NUMBER: US/09/105,907A
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 9
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-105-907-9

Query Match          2.5%; Score 19; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 ATGATGCTGCAATGCGG 289
Db 19 ATGATGCTGCAATGCGG 1
```

Wed Feb 18 12:49:31 2004

us-10-023-182-1.oliszm.rni

Page 6

Db 13 ATGATGCTGCAGATGCCG 31

RESULT 15
US-09-359-503-2
Sequence 2, Application US/09359503
Patent No. 6251603
GENERAL INFORMATION:
APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
APPLICANT: Knuth, Alexander
TITLE OF INVENTION: Method for Determining Status of A
TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
TITLE OF INVENTION: a Patient Sample
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,503
FILING DATE: July 23, 1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/165,546
FILING DATE: October 2, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6251603men D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-359-503-2

Query Match 2.5%; Score 19; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 271 ATGATGCTGCAGATGCCG 289
DB 13 ATGATGCTGCAGATGCCG 31

Search completed: February 17, 2004, 20:15:57
Job time : 75 secs


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/ Sequence 3, Application US/09751798
/ Patent No. US2002010321A1
/ GENERAL INFORMATION:
/ APPLICANT: Stockert, Elisabeth; Jager, Elke;
/ APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
/ APPLICANT: Knuth, Alexander; Old, Lloyd J.
/ TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
/ TITLE OF INVENTION: Associated Proteins, Uses Thereof,
/ TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
/ TITLE OF INVENTION: Binding Peptides Derived Therefrom
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Fulbright & Jaworski, L.L.P.
/ STREET: 666 Fifth Avenue
/ CITY: New York City
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
/ COMPUTER: IBM
/ OPERATING SYSTEM: PC-DOS
/ SOFTWARE: WordPerfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/751,798
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/062,422
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/725,182
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hanson, No. US20020010321A1man D.
/ REGISTRATION NUMBER: 30,946
/ REFERENCE/DOCKET NUMBER: LUD 5466.3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 318-3168
/ TELEFAX: (212) 752-5958
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 32 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-751-798-3

Query Match 2.7%; Score 20; DB 9; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 580 CAGGCGAGGCGGCTAAGCC 599
Db 32 CAGGCGAGGCGGCTAAGCC 13
```

```
RESULT 3
US-10-262-666-18/c
/ Sequence 18, Application US/10262666
/ Publication No. US20030180295A1
/ GENERAL INFORMATION:
/ APPLICANT: Nakayama, Elichi
/ APPLICANT: Ono, Toshio
/ APPLICANT: Old, Lloyd J.
/ APPLICANT: Hasegawa, Kosei
/ APPLICANT: Matsushita, Hirokazu
/ TITLE OF INVENTION: CANCER-TESTIS ANTIGENS
/ FILE REFERENCE: L00461.70140
/ CURRENT APPLICATION NUMBER: US/10/262,666
/ PRIOR APPLICATION NUMBER: PCT/US02/12497
/ PRIOR FILING DATE: 2002-04-19
/ PRIOR APPLICATION NUMBER: US 60/356,937
```

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/ PRIOR FILING DATE: 2002-02-14
/ PRIOR APPLICATION NUMBER: US 60/285,343
/ PRIOR FILING DATE: 2001-04-20
/ NUMBER OF SEQ ID NOS: 80
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 18
/ LENGTH: 32
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Primer
/ US-10-262-666-18

Query Match 2.7%; Score 20; DB 13; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 580 CAGGCGAGGCGGCTAAGCC 599
Db 32 CAGGCGAGGCGGCTAAGCC 13
```

```
RESULT 4
US-10-023-182-3/c
/ Sequence 3, Application US/10023182
/ Publication No. US2002016465A1
/ GENERAL INFORMATION:
/ APPLICANT: Stockert, Elisabeth; Jager, Elke;
/ APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
/ APPLICANT: Knuth, Alexander; Old, Lloyd J.
/ TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
/ TITLE OF INVENTION: Associated Proteins, Uses Thereof,
/ TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
/ TITLE OF INVENTION: Binding Peptides Derived Therefrom
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Fulbright & Jaworski, L.L.P.
/ STREET: 666 Fifth Avenue
/ CITY: New York City
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
/ COMPUTER: IBM
/ OPERATING SYSTEM: PC-DOS
/ SOFTWARE: WordPerfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/023,182
/ FILING DATE: 17-Dec-2001
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/751,798
/ FILING DATE: December 29, 2000
/ APPLICATION NUMBER: LUD 5466.3
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: 08/725,182
/ FILING DATE: October 3, 1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hanson, No. US2002016465A1man D.
/ REGISTRATION NUMBER: 30,946
/ REFERENCE/DOCKET NUMBER: LUD 5466.3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 318-3168
/ TELEFAX: (212) 752-5958
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 32 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 3:
/ US-10-023-182-3
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Query Match 2.7%; Score 20; DB 14; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 580 CAGGGCAGAGCGCGCTAAGCC 599
DB 32 CAGGGCAGAGCGCGCTAAGCC 13

RESULT 5
US-09-751-798-2
Sequence 2, Application US/09751798

PATENT No. US20020010321A1
GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
TITLE OF INVENTION: Associated Proteins, Uses Thereof,
TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US20020010321A1man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-751-798-2

Query Match 2.5%; Score 19; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 ATGATGCTGCAGATGCGG 289
DB 13 ATGATGCTGCAGATGCGG 31

RESULT 6
US-10-262-666-17
Sequence 17, Application US/10262666
Publication No. US20030180298A1
GENERAL INFORMATION:
APPLICANT: Nakayama, Eiichi

APPLICANT: Ono, Toshiro
APPLICANT: Old, Lloyd J.
APPLICANT: Hasegawa, Kohei
APPLICANT: Matsushita, Hirokazu
TITLE OF INVENTION: CANCER-TESTIS ANTIGENS
FILE REFERENCE: L00461.70140
CURRENT APPLICATION NUMBER: US/10/262,666
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: PCT/US02/12497
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/356,937
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/285,343
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 31
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: primer
US-10-262-666-17

Query Match 2.5%; Score 19; DB 13; Length 31;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 ATGATGCTGCAGATGCGG 289
DB 13 ATGATGCTGCAGATGCGG 31

RESULT 7
US-10-023-182-2
Sequence 2, Application US/10023182
Publication No. US20020164655A1

GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
TITLE OF INVENTION: Associated Proteins, Uses Thereof,
TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,182
FILING DATE: 17-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/751,798
FILING DATE: December 29, 2000
APPLICATION NUMBER: 09/062,422
FILING DATE: <unknown>
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US20020164655A1man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-023-182-2

Query Match 2.5%; Score 19; DB 14; Length 31;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 ATGATGCTGCAGATGCGG 289
DB 13 ATGATGCTGCAGATGCGG 31

RESULT 8
US-10-194-370-39
Sequence 39, Application US/10194370
Publication No. US20030096270A1
GENERAL INFORMATION:

APPLICANT: Paul Andrew Whitaker et al
TITLE OF INVENTION: Disease-Associated Gene
FILE REFERENCE: Case 4-32067A/HO 41
CURRENT FILING DATE: 2002-07-12
NUMBER OF SEQ ID NOS: 94
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 39
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-10-194-370-39

Query Match 2.4%; Score 18; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 623 CAGCTCTCTCCCTAGG 640
DB 4 CAGCTCTCTCCCTAGG 21

RESULT 9
US-10-423-399-78/c
Sequence 78, Application US/10423399
Publication No. US20040005605A1
GENERAL INFORMATION:

APPLICANT: Hino, Akihito
APPLICANT: Matsuoka, Takeshi
APPLICANT: Kuribara, Hideo
APPLICANT: Yoshimura, Tomoaki
APPLICANT: Shindo, Yoichihiro
APPLICANT: Futo, Satoshi
APPLICANT: Ogawa, Masahiko
TITLE OF INVENTION: Methods of Quantitative Detection of Genetic Recombinants and
TITLE OF INVENTION: Standard Molecules for the Methods
FILE REFERENCE: 1285-5 PCT/US
CURRENT APPLICATION NUMBER: US/10/423,399
CURRENT FILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: PCT/JP01/09344
PRIOR FILING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.2
SEQ ID NO 78
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: PCR primer
US-10-423-399-78

Query Match 2.1%; Score 16; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 5,1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 495 TCCATCAGCTCTCTGC 510
DB 16 TCCATCAGCTCTCTGC 1

RESULT 10
US-10-349-143-1665
Sequence 1665, Application US/10349143
Publication No. US20040005584A1
GENERAL INFORMATION:

APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Ballelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CPI
CURRENT APPLICATION NUMBER: US/10/349,143
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: US/09/422,978
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 1665
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 99-5472-290 : polymorphic base C or T
US-10-349-143-1665

Query Match 2.1%; Score 16; DB 12; Length 47;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CTGACCTTCTCTCTGA 29
DB 2 CTGACCTTCTCTCTGA 17

RESULT 11
US-10-168-789A-19/c
Sequence 19, Application US/10168789A
Publication No. US20030148943A1
GENERAL INFORMATION:
APPLICANT: Nishi, Kazunori
APPLICANT: Itoh, Yasuaki
APPLICANT: Kitada, Chieko
APPLICANT: INATOMI, No. US20030148943A1
TITLE OF INVENTION: No. US20030148943A1 Tachykinin-like Polypeptides and Use Thereo
FILE REFERENCE: 2680USOP
CURRENT APPLICATION NUMBER: US/10/168,789A
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: PCT/JP00/09083
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: JP 11-362638
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: JP 12-066714
PRIOR FILING DATE: 1999-03-10
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 19

LENGTH: 93
TYPE: DNA
ORGANISM: human
US-10-168-789A-19

Query Match
Best Local Similarity 2.1%; Score 16; DB 13; Length 93;
100.0%; Pred. No. 4.8e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 GCCCAGAGAGCCCTG 118
DB 71 GCCCAGAGAGCCCTG 56

RESULT 12
US-10-178-325-91/C
Sequence 91, Application US/10178325
Publication No. US2003019467A1
GENERAL INFORMATION:
APPLICANT: Robert, M. Luisa
APPLICANT: Cowsett, Lex M.
TITLE OF INVENTION: Antisense Modulation of Human Rho Family Gene
FILE REFERENCE: ISPH-0404
CURRENT APPLICATION NUMBER: US/10/178,325
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US/09/387,341
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 09/156,424
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 09/156,979
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 09/156,807
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 09/161,015
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 233
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 91
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-178-325-91

Query Match
Best Local Similarity 2.0%; Score 15; DB 13; Length 18;
100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 CAGAGCTGCCCCGCA 372
DB 15 CAGAGCTGCCCCGCA 1

RESULT 13
US-10-084-839-3696
Sequence 3696, Application US/10084839
Publication No. US20030186238A1
GENERAL INFORMATION:
APPLICANT: Third Wave Technologies
APPLICANT: Allawi, Hatim
APPLICANT: Argue, Brad T.
APPLICANT: Bartholomew, Christian T.
APPLICANT: Chehak, LuAnne
APPLICANT: Curtis, Michelle L.
APPLICANT: Eis, Peggy S.
APPLICANT: Hall, Jeff G.
APPLICANT: Ip, Hon S.
APPLICANT: Ji, Lin
APPLICANT: Kaiser, Michael
APPLICANT: Kwiatkowski, Jr., Robert W.
APPLICANT: Lukowiak, Andrew A.

APPLICANT: Lyamichev, Victor
APPLICANT: Lyamicheva, Natalie E.
APPLICANT: Ma, Mupo
APPLICANT: Neri, Bruce P.
APPLICANT: Olson, Sarah M.
APPLICANT: Olson-Munoz, Marilyn C.
APPLICANT: Schaefer, James J.
APPLICANT: Skrzypczynski, Zdzigniew
APPLICANT: Takova, Tsetska Y.
APPLICANT: Thompson, Lisa C.
APPLICANT: Vedyik, Kevin L.
TITLE OF INVENTION: RNA Detection Assays
FILE REFERENCE: FORS-06666
CURRENT APPLICATION NUMBER: US/10/084,639
CURRENT FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 4004
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3696
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-084-839-3696

Query Match
Best Local Similarity 2.0%; Score 15; DB 13; Length 21;
100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 656 GAGTGCCAGTTTCAT 670
DB 5 GAGTGCCAGTTTCAT 19

RESULT 14
US-10-084-839-3720
Sequence 3720, Application US/10084839
Publication No. US20030186238A1
GENERAL INFORMATION:
APPLICANT: Third Wave Technologies
APPLICANT: Allawi, Hatim
APPLICANT: Argue, Brad T.
APPLICANT: Bartholomew, Christian T.
APPLICANT: Chehak, LuAnne
APPLICANT: Curtis, Michelle L.
APPLICANT: Eis, Peggy S.
APPLICANT: Hall, Jeff G.
APPLICANT: Ip, Hon S.
APPLICANT: Ji, Lin
APPLICANT: Kaiser, Michael
APPLICANT: Kwiatkowski, Jr., Robert W.
APPLICANT: Lukowiak, Andrew A.
APPLICANT: Lyamichev, Victor
APPLICANT: Lyamicheva, Natalie E.
APPLICANT: Ma, Mupo
APPLICANT: Neri, Bruce P.
APPLICANT: Olson, Sarah M.
APPLICANT: Olson-Munoz, Marilyn C.
APPLICANT: Schaefer, James J.
APPLICANT: Skrzypczynski, Zdzigniew
APPLICANT: Takova, Tsetska Y.
APPLICANT: Thompson, Lisa C.
APPLICANT: Vedyik, Kevin L.
TITLE OF INVENTION: RNA Detection Assays
FILE REFERENCE: FORS-06666
CURRENT APPLICATION NUMBER: US/10/084,839
CURRENT FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 4004
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3720
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Synthetic
US-10-084-839-3720

Query Match 2.0%; Score 15; DB 13; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 656 GAGTGGCCAGTTTCAT 670
DB 5 GAGTGGCCAGTTTCAT 19

RESULT 15
US-10-084-839-3724
Sequence 3724, Application US/10084839
Publication No. US20030186238A1
GENERAL INFORMATION:
APPLICANT: Third Wave Technologies
APPLICANT: Alawi, Hatim
APPLICANT: Argue, Brad T.
APPLICANT: Bartholomew, Christian T.
APPLICANT: Chehak, Lubane
APPLICANT: Curtis, Michelle L.
APPLICANT: Eis, Peggy S.
APPLICANT: Hall, Jeff G.
APPLICANT: Ip, Hon S.
APPLICANT: Ji, Lin
APPLICANT: Kaiser, Michael
APPLICANT: Kwiatkowski, Jr., Robert W.
APPLICANT: Lukowiak, Andrew A.
APPLICANT: Lyamichev, Victor
APPLICANT: Lymaicheva, Natalie E.
APPLICANT: Ma, Mupo
APPLICANT: Neel, Bruce P.
APPLICANT: Olson, Sarah W.
APPLICANT: Olson-Munoz, Marilyn C.
APPLICANT: Schaefer, James J.
APPLICANT: Skrzypczynski, Zbigniew
APPLICANT: Takova, Tsetska Y.
APPLICANT: Thompson, Lisa C.
APPLICANT: Vedvik, Kevin L.
TITLE OF INVENTION: RNA Detection Assays
FILE REFERENCE: FORS-06666
CURRENT APPLICATION NUMBER: US/10/084,839
CURRENT FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 4004
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3724
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-084-839-3724

Query Match 2.0%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 656 GAGTGGCCAGTTTCAT 670
DB 5 GAGTGGCCAGTTTCAT 19

Search completed: February 17, 2004, 21:28:52
Job time: 364 secs

Wed Feb 18 12:49:31 2004

us-10-023-182-1.clisizm.rst

Page 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 17, 2004, 18:07:19 / Search time 2450 Seconds

(without alignments)
7459.986 Million cell updates/sec

Title: US-10-023-182-1

Perfect score: 752

Sequence: 1 ATCCCTGCTGGCCCTGACCT.....TAAACTGAGCTACGAAAA 752

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size: 0

Total number of hits satisfying chosen parameters: 452990

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database:

EST:
1: em_estda:
2: em_estm:
3: em_estm:
4: em_estm:
5: em_estm:
6: em_estm:
7: em_estm:
8: em_estm:
9: gb_est1:
10: gb_est2:
11: gb_est3:
12: gb_est4:
13: gb_est5:
14: gb_est6:
15: em_estfun:
16: em_estfun:
17: em_gss_hum:
18: em_gss_hum:
19: em_gss_hum:
20: em_gss_hum:
21: em_gss_hum:
22: em_gss_hum:
23: em_gss_hum:
24: em_gss_hum:
25: em_gss_hum:
26: em_gss_hum:
27: em_gss_hum:
28: gb_gss1:
29: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARYS

Result No.	Score	Query Match Length	ID	Description
1	2.3	53	AZ466360	AZ466360 IM0277E04
2	2.1	84	A1305415	A1305415 gw72h07.x
3	2.1	94	AA628968	AA628968 af28h08.s
4	2.1	94	A1305911	A1305911 gw73g08.x

5	15	2.0	42	29	AL943490	AL943490 Arabidops
6	15	2.0	43	14	H24505	H24505 y13h03.x1
7	15	2.0	59	28	AZ410004	AZ410004 IM0182F04
8	15	2.0	61	9	AW029421	AW029421 wx11d06.x
9	15	2.0	65	12	B1872120	B1872120 6033963428
10	15	2.0	67	12	B1872041	B1872041 603396336
11	15	2.0	75	10	BF725764	BF725764 bx19f03.y
12	15	2.0	76	9	AA654397	AA654397 nt03e11.s
13	15	2.0	77	10	BP245390	BP245390 601863678
14	15	2.0	82	14	R83718	R83718 ypl5a09.x1
15	15	2.0	82	29	EX225420	EX225420 Danio rer
16	15	2.0	88	9	AA474534	AA474534 v934e02.x
17	15	2.0	91	28	AZ646945	AZ646945 IM0513010
18	15	2.0	94	28	AZ822068	AZ822068 2M0095D02
19	15	2.0	94	29	B2356067	B2356067 SALX 1280
20	15	2.0	96	10	BE493292	BE493292 WHE0571.A
21	15	2.0	97	9	AA953544	AA953544 cm79g06.s
22	15	2.0	99	6	AL811457	AL811457 Tricicum
23	15	2.0	100	9	AA485597	AA485597 t126c07.x
24	15	2.0	100	14	R99501	R99501 yq71g09.x1
25	14	1.9	31	9	AF171909	AF171909 as47f06.x
26	14	1.9	31	10	BF181705	BF181705 601805518
27	14	1.9	31	14	H62630	H62630 yr43d07.x1
28	14	1.9	34	9	A1378501	A1378501 tcs6h07.x
29	14	1.9	34	9	A1544482	A1544482 fb75e12.x
30	14	1.9	40	9	AA730831	AA730831 mw49f05.s
31	14	1.9	40	14	W19905	W19905 db38c04.x1
32	14	1.9	43	9	AA746857	AA746857 mx64c03.s
33	14	1.9	43	9	AA209506	AA209506 z035c01.x
34	14	1.9	46	9	AA652871	AA652871 ns75e09.s
35	14	1.9	46	9	A1124043	A1124043 q849g11.s
36	14	1.9	47	28	AZ768968	AZ768968 IM0569P09
37	14	1.9	48	28	AZ481547	AZ481547 IM0303D20
38	14	1.9	49	9	AA334271	AA334271 SMOVL3CAN
39	14	1.9	49	9	AA225066	AA225066 nc34f10.x
40	14	1.9	49	9	AA531157	AA531157 nj48d01.s
41	14	1.9	49	9	AA569761	AA569761 nt25f04.s
42	14	1.9	49	14	T59469	T59469 yb63d05.x1
43	14	1.9	50	9	AU102241	AU102241 AU102241
44	14	1.9	50	9	AU105932	AU105932 AU105932
45	14	1.9	50	9	AU105934	AU105934 AU105934

ALIGNMENTS

RESULT 1
LOCUS
DEFINITION
clone UGCLM0277E04 F, genomic survey sequence.

ACCESSION
AZ466360
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: dmunogenetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0277 row: E column: 04
 Seq primer: CGTGTAAACGACGCCAGCT
 Class: plasmid ends
 High quality sequence stop: 53.
 Location/Qualifiers

1. 53
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG1M0277E04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUCG1M library"
 /note="Vector: pMD42uv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

15 a 14 c 17 g 7 t

ORIGIN

Query Match 2.3%; Score 17; DB 28; Length 53;
 Best Local Similarity 100.0%; Pred. No. 1 ee+03;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 GCCCTGGCATTCTCTGAT 128

DB 51 GCCCTGGCATTCTCTGAT 35

RESULT 2
 AI1305415/c 84 bp mRNA linear EST 09-DEC-1998
 LOCUS qw71h07.x1 NCI_CGAP_OV33 Homo sapiens cDNA clone IMAGE:196573 3,
 DEFINITION mRNA sequence.

ACCESSION AI1305415

VERSION AI1305415.1 GI:3990306

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 84)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 CDNA Library Preparation: David B. Krizman, Ph.D.
 CDNA Library Arrayed by: I.M.A.G.E. Consortium, LNL
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/INLNL at:
 www.bio.lnlnl.gov/btrp/image/image.html
 Seq primer: -40up from Gibco

JOURNAL COMMENT

High quality sequence stop: 53.
 Location/Qualifiers

1. 84
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:196573"
 /sex="female"
 /tissue_type="borderline ovarian carcinoma"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP OV33"
 /note="Organ: ovary; Vector: pAMP1; mRNA made from borderline ovarian carcinoma, cDNA made by oligo-dt priming. Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified."

BASE COUNT

46 a 8 c 23 g 7 t

ORIGIN

Query Match 2.1%; Score 16; DB 9; Length 84;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 511 TCCAGCAGCTTCCCT 526

DB 61 TCCAGCAGCTTCCCT 46

RESULT 3
 AA628968/c 94 bp mRNA linear EST 02-MAR-1998
 LOCUS af28h08.s1 Soares total fetus Nb2HP8 9w Homo sapiens cDNA clone
 DEFINITION IMAGE:1033023 3 similar to R:G762951 G762951 PRP-2 PROTEIN
 ; contains element TARI repetitive element ; mRNA sequence.

ACCESSION AA628968

VERSION AA628968.1 GI:2541355

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 94)
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Martin, M.,
 Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
 White, Y., Wylie, T., Waterston, R. and Wilson, R.
 WashU-NCI human EST project
 Unpublished
 Contact: Wilson R.
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnlnl.gov) for further information.
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Insert Length: 776 Std Error: 0.00
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source

1. 94
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1033023"
 /dev_stage="8-9 weeks"
 /lab_host="DH10B"
 /clone_lib="Soares total fetus Nb2HP8 9w"
 /note="Vector: pT73d-Pac (Pharmacia) with a modified
 polylinker, site_1: Not I; site_2: Eco RI; 1st strand cDNA

was prepared from mRNA obtained from pooled 8-9 week (total) fetus material with a Not I - Clisg(dT) primer [5', GTTACCACTGAGTGGAGCGCCCTTAATTTTCTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTV3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo.

BASE COUNT

25 a 33 c 30 g 6 t

Query Match 2.1%; Score 16; DB 9; Length 94;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

186 CCCCCGGGGGGGCGAGGG 201
77 CCCCCGGGGGGGCGAGGG 62

RESULT 4
A1305911 94 bp mRNA linear EST 09-DEC-1998
LOCUS gw73908.x1 NCI_CGAP_Ov33 Homo sapiens cDNA clone IMAGE:1996766 3',
DEFINITION mRNA sequence.

ACCESSION A1305911 GI:3989040
VERSION A1305911
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE 1 (bases 1 to 94)
Nucleotide sequence of the human cDNA clone gw73908.x1, NCI-CGAP project (CGAP), National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgs@nsl.nhlbi.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrived by: I.M.A.G.E. Consortium, LNL
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
www.dio.lnl.gov/dbp/image/image.html
Seq primer: -40UP from Gibco.

FEATURES
source
1..94
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1996766"
/sex="female"
/tissue_type="borderline ovarian carcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1ib="NCI CGAP Ov33"
/note="Organ: ovary; Vector: pAMP1; mRNA made from borderline ovarian carcinoma. cDNA made by oligo-dT priming. Directionally cloned. Size selected on agarose gel, average insert size 500 bp. Primary library, non-amplified."

BASE COUNT 48 a 10 c 26 g 10 t

Query Match 2.1%; Score 16; DB 9; Length 94;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

511 TCCAGCAGCTTCCCT 526
61 TCCAGCAGCTTCCCT 46

RESULT 5
AL943490 42 bp DNA linear GSS 24-OCT-2002
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-274G08-015094,
DEFINITION genomic survey sequence.

ACCESSION AL943490 GI:24400088
VERSION AL943490
KEYWORDS GSS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Strizhov, N., Li, Y., Rosso, M., Viehovec, P., Dekker, K., Saedler, H.
TITLE A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines

JOURNAL
REFERENCE 2
AUTHORS Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weissshaar, B.
TITLE A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics

JOURNAL
REFERENCE 3 (bases 1 to 42)
AUTHORS Strizhov, N., Rosso, M., Li, Y. and Weissshaar, B.
TITLE Direct Submission
COMMENT Submitted (21-OCT-2002) Weissshaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone F10C21. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/

FEATURES
source
1..42
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-274G08-015094"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

BASE COUNT 9 a 12 c 2 g 19 t

Query Match 2.0%; Score 15; DB 29; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

14 CTGACCTTCTCTCTG 28
8 CTGACCTTCTCTCTG 22

RESULT 6
LOCUS H24505 43 bp mRNA linear EST 06-JUL-1995
DEFINITION Y130h03.r1 Soares breast 3Ndbst Homo sapiens cDNA clone IMAGE:159797 5' similar to SP:S29539 S29539 BASIC PROTEIN, 23K - ;, mRNA sequence.

ACCESSION H24505
 VERSION H24505.1 GI:893200
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 43)
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Ellington, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wondolam, P. and Wilson, R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Insert Size: 760
 High quality sequence starts: 1
 High quality sequence stops: 1
 Source: IMAGE Consortium, LBNL
 This clone is available royalty-free through LBNL; contact the IMAGE Consortium (info@image.lbnl.gov) for further information.
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Insert Length: 760 Std Error: 0.00
 Seq primer: M13Rev
 High quality sequence stop: 1.
 Location/Qualifiers
 1. 43
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:578180"
 /db_xref="taxon:9606"
 /clone="IMAGE:159797"
 /sex="Female"
 /dev_stage="adult"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares breast 3NdbHst"
 /note="Organ: breast; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo (dT) primer [5' TGTTACCATCTGAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M. Fatima Bonaldi."

BASE COUNT 15 a 9 c 7 g 12 t
 ORIGIN
 Query Match 2.0%; Score 15; DB 14; Length 43;
 Best Local Similarity 100.0%; Pred. No. 1.7e+04;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 717 TTGTTCTGTGAGAA 731
 DB 40 TTGTTCTGTGAGAA 26

RESULT 7
 AZ410004 59 bp DNA linear GSS 03-OCT-2000
 LOCUS AZ410004
 DEFINITION 1M0182204F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 accession AZ410004
 version AZ410004.1 GI:10534017
 keywords GSS.
 source Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 59)
 AUTHORS Dunn, P., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112 USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0182 row: F column: 04
 Seq primer: CGTGTAAACGACGCCACT
 Class: plasmid ends
 High quality sequence stop: 59.
 Location/Qualifiers
 1. 59
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0182F04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (914732114bp|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 10 a 24 c 10 g 15 t
 ORIGIN
 Query Match 2.0%; Score 15; DB 28; Length 59;
 Best Local Similarity 100.0%; Pred. No. 1.9e+04;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 110 AGGCCCTTGCAATTC 124
 DB 27 AGGCCCTTGCAATTC 41

RESULT 8
 AM029421 61 bp mRNA linear EST 15-SEP-1999
 LOCUS AM029421
 DEFINITION wx11d06.x1 NCI CGAP_Gas4 Homo sapiens cDNA IMAGE:2543359 3',
 accession AM029421
 version AM029421.1 GI:5888177
 keywords EST.
 source

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 61)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R. Emmer-Buck, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
 Seq primer: -40UP from GIBCO
 High quality sequence, stop: 50.
 Location/Qualifiers

FEATURES
 source
 1..61
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2543339"
 /tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Gas4"
 /note="Organ: stomach; Vector: PCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally; Primer: Oligo dt. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"

BASE COUNT 16 a 11 c 19 g 15 t

ORIGIN

Query Match 2.0%; Score 15; DB 9; Length 61;
 Best Local Similarity 100.0%; Pred. No. 1.9e+04;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 CCCAGAGAGCCCTGG 118
 DB 37 CCCAGAGAGCCCTGG 51

RESULT 9
LOCUS B1872120 65 bp mRNA linear EST 11-OCT-2001
DEFINITION 603396428P1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5400223 5', mRNA sequence.
ACCESSION B1872120
VERSION B1872120.1 GI:16045795
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 65)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: L1AM12020 row: 9 column: 08

FEATURES High quality sequence stop: 65.
 Location/Qualifiers
 source
 1..65
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:5400223"
 /tissue_type="retina"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_94"
 /note="Organ: eye; Vector: PCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dt primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

BASE COUNT 11 a 24 c 16 g 14 t

ORIGIN

Query Match 2.0%; Score 15; DB 12; Length 65;
 Best Local Similarity 100.0%; Pred. No. 1.9e+04; *
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 GCGCCAGAGGCGCCT 116
 DB 34 GCGCCAGAGGCGCCT 20

RESULT 10
LOCUS B1872041 67 bp mRNA linear EST 11-OCT-2001
DEFINITION 603396316P1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5400224 5', mRNA sequence.
ACCESSION B1872041
VERSION B1872041.1 GI:16045716
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 67)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: L1AM12020 row: 9 column: 09
 High quality sequence stop: 67.
 Location/Qualifiers

FEATURES
 source
 1..67
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:5400224"
 /tissue_type="retina"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_94"
 /note="Organ: eye; Vector: PCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dt primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

BASE COUNT 11 a 24 c 17 g 15 t

ORIGIN

Query Match 2.0%; Score 15; DB 12; Length 67;
 Best Local Similarity 100.0%; Pred. No. 2e+04;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 102 GGCCGAGAGGCCCT 116
 DB 36 GGCCGAGAGGCCCT 22

RESULT 11
 BF725764/c

75 bp mRNA linear EST 05-JAN-2001

LOCUS bxl19f03.y1 Human Iris cDNA (Un-normalized, unamplified); EX Homo
 DEFINITION sapiens cDNA clone bxl19f03 5', mRNA sequence.

ACCESSION BF725764
 VERSION BF725764.1 GI:12041675

KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE Wiscow,G.U., Bernstein,S., Behal,A. and Smith,D.
 1 (bases 1 to 75)

AUTHORS NEIBANK: EST analysis and bioinformatics for ocular genomics
 JOURNAL Invest. Ophthalmol. Vis. Sci. 41, (2000) In press
 COMMENT Contact: Wiscow G

Section on Molecular Structure and Function
 National Eye Institute
 6/331, NIH, Bethesda, MD 20892-2740, USA

Tel: 301 402 3452
 Fax: 301 496 0078

Email: graham@helix.nih.gov
 Plate: 19 row: f column: 03

Seg primer: M13P1 reverse primer (ABI).
 Location/Qualifiers

1..75
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="bx19f03"
 /tissue_type="iris"
 /dev_stage="Adult"
 /lab_host="EMD10B"
 /clone_lib="Human Iris cDNA (Un-normalized, unamplified):
 EX"

/note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris
 tissue was pooled from 10 individuals ranging in age from
 4-80 years and RNA was extracted. From this pooled sample
 an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A
 directionally cloned cDNA library in the pCMVSPORT6 vector
 was constructed at Life Technologies, essentially
 following the protocols of the Superscript Plasmid System
 full details of which are contained in the manufacturer's
 instruction manual (http://www.lifetech.com/). First
 strand synthesis was carried out using a Not I
 primer-adaptor (5'-GCACTAGTCTGATCGGAGCGGCCCT)15-3'.
 1. Not I/blunt end inserts were cloned into the Not I/EcoR
 V sites in the vector. EST analysis was performed on the
 unamplified library at the NIH Intramural Sequencing
 Center (NISC)."

BASE COUNT 21 a 15 c 20 g 19 t
 ORIGIN

Query Match 2.0%; Score 15; DB 10; Length 75;
 Best Local Similarity 100.0%; Pred. No. 2e+04;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 717 TTGTTCTGTAGAA 731
 DB 63 TTGTTCTGTAGAA 49

RESULT 12
 AA654397 76 bp mRNA linear EST 23-DEC-1997

DEFINITION

nt0311.e1 NCI CGAP Lym3 Homo sapiens cDNA clone IMAGE:1192076 3',
 similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;, mRNA
 sequence.

ACCESSION AA654397
 VERSION AA654397.1 GI:2590551
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 1 (bases 1 to 76)

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
 MARRIN: There is evidence that suggests that the 384-well parent
 plate of this clone contains both human and mouse derived clones.
 Thus, the origin of this clone is uncertain. This caution should be
 kept in mind should you use this clone.

Tissue Procurement: Mark Raffeld, M.D., Michael R. Emmert-Buck,
 M.D., Ph.D.
 cDNA Library Preparation: Stratagene, Inc., David B. Kitzman,
 Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
 www.bto.linl.gov/btrp/image/image.html

Trace considered overall poor quality
 Insert Length: 899 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 1.

FEATURES

source

1..76
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1192076"
 /tissue_type="lymphoma"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="NCI CGAP Lym3"
 /note="Organ: lymph node; Vector: Bluescript SK-; Site: 1:
 ESCR1; Site 2: XhoI; Cloned unidirectionally. Primer:
 Oligo dT. Pooled lymphomas. 5' adaptor sequence: 5'
 GAATTCGGACGAG 3' 3' adaptor sequence: 5'
 CTCGAGTTTCTTTTCTTTTCTTTT 3' Average insert size: 0.9 kb."

BASE COUNT 21 a 19 c 14 g 22 t
 ORIGIN

Query Match 2.0%; Score 15; DB 9; Length 76;
 Best Local Similarity 100.0%; Pred. No. 2e+04;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 717 TTGTTCTGTAGAA 731
 DB 18 TTGTTCTGTAGAA 32

RESULT 13
 BF245390/c 77 bp mRNA linear EST 14-NOV-2000
 LOCUS 601861678P1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:408115 5',
 mRNA sequence.

DEFINITION BF245390
 ACCESSION BF245390.1 GI:11159323

KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 77)
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Sequencing by: InCyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: L1CM942 row: 1 column: 20
 High quality sequence stop: 77.

FEATURES

source

1..77
 Location/Qualifiers

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4081315"
 /tissue_type="glioblastoma"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC 57"
 /note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
 SfiI (ggcgccgcgcgc); Site_2: SfiI (ggcgccgcgcgc);
 Double-stranded cDNA was prepared from cell line RNA. 5'
 and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CACGGCATTATGCGC-3' and 3' adaptor
 sequence: 5'-ATTCTAGAGCGCGCGCGCAGCATG-dT(30)B-3'
 (where B = A, C, G, or T). Average
 insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA)."

BASE COUNT

8 a 29 c 22 g 18 t

Query Match 2.0%; Score 15; DB 10; Length 77;
 Best Local Similarity 100.0%; Pred. No. 2e+04;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGAGCTGGCGCCGAG 373

DB 40 AGAGCTGGCGCCGAG 26

RESULT 14 82 bp mRNA linear EST 04-AUG-1995
 R83718
 LOCUS YP15A09.k1 Soares breast 3MbHst Homo sapiens CDNA clone
 IMAGE:187480.5 similar to SP1A4367 P23-TUMOR-SPECIFIC
 TRANSCRIPTION ANTIGEN P198 HOMOLOG - BOVINE ; mRNA sequence.

DEFINITION R83718

ACCESSION R83718.1 GI:928595

VERSION R83718

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 82)
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman,
 M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
 Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston,
 R., Williamson, A., Woldmann, P. and Wilson, R.
 The Washu-Merck EST Project
 Unpublished
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

TITLE

JOURNAL COMMENT

FEATURES

source

1..82
 Location/Qualifiers

/organism="Danio rerio"
 /mol_type="genomic DNA"
 /db_xref="taxon:7955"
 /clone="DKEY-254G21"

Email: esr@watson.wustl.edu

Insert Size: 721

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Possible reversed clone; similarity on wrong strand

Insert Length: 721 Std Error: 0.00

Seq primer: M13RPI

High quality sequence stop: 1.

Location/Qualifiers

1..82
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:3818376"
 /db_xref="taxon:9606"
 /clone="IMAGE:187480"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: breast; Vector: pT73D (Pharmacia) with a
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
 strand cDNA was primed with a Not I - cTGGG(dT) primer [5'
 TGTTCATCTGAGTGGAGCGCGCGCCCTTTTCTTTTCTTTT 3']
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of a modified pT73 vector (Pharmacia).
 Library went through one round of normalization to a Cot =
 20. Library constructed by Bento Soares and M. Fatima
 Bonaldo."

BASE COUNT

21 a 15 c 18 g 23 t 5 others

Query Match 2.0%; Score 15; DB 14; Length 82;
 Best Local Similarity 100.0%; Pred. No. 2.1e+04;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 717 TTGTTCTGTAGAAA 731

DB 63 TTGTTCTGTAGAAA 49

RESULT 15 82 bp DNA linear GSS 29-JAN-2003
 BX225420
 LOCUS Danio rerio genomic clone DKEY-254G21, genomic survey sequence.

DEFINITION BX225420

ACCESSION BX225420.1 GI:28059508

VERSION GSS.

KEYWORDS Danio rerio (zebrafish)

SOURCE Danio rerio

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 82)
 Humphray, S.J., Huckle, E. and Durham, J.L.
 Direct Submission
 Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
 Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humphray@sanger.ac.uk Unpublished

This sequence was generated from the 77 end of BAC 254G21. 254G21
 is part of the Daniokey BAC library created by R. Plasterk and N.V.
 Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.

COMMENT

AUTHORS

JOURNAL

Wed Feb 18 12:49:31 2004

us-10-023-182-1.01szlm.rst

Page 8

/tissue_type="Testis"
/note="vector pindigobac-536"
BASE COUNT 25 a 10 c 45 g 2 t
ORIGIN

Query Match 2.0%; Score 15; DB 29; Length 82;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 CCTTGGCGACACCC 350
|||
Db 28 CCTTGGCGACACCC 14

Search completed: February 17, 2004, 20:14:35
Job time : 2458 secs